



SEQUENCE LISTING

<110> Joshua Z. Levin
Ken Phillips
Greg Budziszewski
Fred Meins
Zhenya Glazov

<120> Methods of Controlling Gene Expression

<130> 31481USNP

<140> 09/896,186

<141> 2001-06-29

<150> 60/222,202

<151> 2000-08-01

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 942

<212> DNA

<213> Arabidopsis thaliana

<400> 1

```
atgtcatcgt caaattggat cgacgacgct tttacagagg aagagcttct cgctatcgac 60
gccatcgaag cttcctacaa tttctcccgt tcttcttctt cttcttcctc tgctgctccg 120
accgtacaag ctacaacctc cgtccatggc cagcaggagg atccaaatca aatccccaat 180
aatatccgtc gccaatggcc tcgttccatc acttcttcta catcttataa acgatttcct 240
ctctcccgtt gccgagctag gaattttcca gcaatgaggt ttgggtggtag gattttgtat 300
agcaagactg ctactgaggt tgataagcga gcaatgcagc ttattaaagt tcttgatacc 360
aagagagatg aatctggaat agcttttgtt ggcttggata ttgagtggag accaagtttt 420
agaaaagggt ttctcccggg gaagggttgcg actgtccaga tatgtgtaga tagtaattat 480
tgtgatgtta tgcataatttt tcattctggt atccctcaaa gtctccaaca tcttattgaa 540
gattcaacac ttgtaaagggt aggtattgga attgatggtg actctgtgaa gcttttccat 600
gactatggag ttagtatcaa agatgttgag gatctttcag atttagccaa ccaaaaaatt 660
ggtggagata aaaaatgggg ccttgccatc ctaactgaga cacttggttg caaagagctc 720
ctgaagccaa acagaatcag gcttggaac tgggagtttt atcctctgtc aaagcagcag 780
ttacaatacg cagcaacgga tgcttatgct tcatggcatc tttacaaggt aacaacaacg 840
aaaaaccatc ttctcacact caacgacctt gaagcaaaaa tctcacatcg ttctaattat 900
aatactgtta cttgtcgaaa acctggaggt tatcttcggt ga 942
```

<210> 2

<211> 313

<212> PRT

<213> Arabidopsis thaliana

<400> 2

```
Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
  1             5             10             15
```

```
Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
      20             25             30
```

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
 35 40 45
 His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
 50 55 60
 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
 65 70 75 80
 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
 85 90 95
 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
 100 105 110
 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
 115 120 125
 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
 130 135 140
 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
 145 150 155 160
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
 165 170 175
 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
 180 185 190
 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
 195 200 205
 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
 210 215 220
 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
 225 230 235 240
 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
 245 250 255
 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
 260 265 270
 His Leu Tyr Lys Val Thr Thr Thr Lys Asn His Leu Leu Thr Leu Asn
 275 280 285
 Asp Leu Glu Ala Lys Ile Ser His Arg Ser Asn Tyr Asn Thr Val Thr
 290 295 300
 Cys Arg Lys Pro Gly Gly Tyr Leu Arg
 305 310

<210> 3

<211> 1929
 <212> DNA
 <213> Arabidopsis thaliana

<400> 3

```

atgagatttg atgatcccat ggatgagttc aagaggaatc gaaagatgga ggaagattcg 60
aagaaggtaa tcgatgtgaa agtggctgag agtgataagg gattcgcgaa atttggcaag 120
gcagaggttc cgtttcatat accgacgtta acgaagcctc aagaggagta taagattttg 180
gtagacaatg ctaataatcc ttttgagcat gttttgttgg agaagagtga agacggtctt 240
cggttcattc atccactgga ggaactatct gtgatggact ttgttgatag aaatctaagt 300
gagatgagac ctgttaagcc tctcccattg gaagagactc cattcaagct agttgaagaa 360
gtcaaaagat ttgaggactt agctgctgca ttgcaaaagt ttgaagagtt tgctgtcgat 420
ctggagcata atcagtatag aacttttcaa ggattaacat gcttgatgca aatctctact 480
agaaccgagg atttatattgt tgatatattc aagctttggg atcacattgg tccttatcta 540
agggaaactct tcaaagaccc taaaaagaaa aaggtaatcc atggagcaga tcgagatatt 600
at ttggcttc aacgggactt tggcatttat gtctgcaatc tttttgacac aggacaggct 660
tcaagggtgc taaagctgga gagaaatagt ctggaatttc ttctgaagca ttattgtgga 720
gttgctgcaa acaaagaata ccaaaaagca gactggagaa taagaccctt tccagatgta 780
atgaaaagat atgctagaga agatacacat tatcttttgt acatttatga tgtaatgcga 840
atggagttgc acacaatggc aaaggaagat gagcaatctg actctcctct ggtagagggtg 900
tacaagcgca gttatgacgt gtgcatgcaa ctatatgaaa aagagctttg gactagggat 960
tcatatcttc acgtttatgg gggttcagaca ggtaatctca atgcggttca actttccatt 1020
gttgcgctgc aggggctttg tgaatggcgg gatcggattg cacgcgcaga tgatgagagc 1080
accggttatg tattgccaaa taaaactctt tttgacatag ccaaggagat gccaatgtgt 1140
gttgcccagt tgcgccgttt gttgaagtca aagcttcctt acctcgagcg taattttgac 1200
gcagtgatca gtgtcatcag acgatcaatg caaaatgcag cggcattcga gccagttgtt 1260
caatctttga aagataggcg tcctgaaaca gtggttgaaa tgaatataga acctaaagatt 1320
gagaaaacag acacaggagc ttcagcgtct tctctgagtc tggagaaggt ttgtgtggat 1380
gattcaaaga aacaaagcag tggtttttga gttttgccgt taaagaggaa gttggaaagt 1440
gacaaaacgg tggttgaaaa gaatatcgaa cctaagattg agaaaacagg cacagaagct 1500
tcagcttctt ctctgagttc gaagaaggtt tgtgtggatg attcaaagaa acaaagcagt 1560
ggttttggag ttttgctgtc aaagaggaag tttgaaagtg ataacaagaa gttgcaggta 1620
aaagaagagg tcaaagtgtc caagtccaag ccagataagg taatcatagt ggtggatgat 1680
gatgatgatg atgatgatga tgagtcttat gaacagagca cgaaagccgc tgatgctttg 1740
gacagagttt cggaacgcc ttcgaaggga tcaccatcgt tgactcaaaa gccgaagaca 1800
tgtaatacag aggttattgt gttagacgat gatgatgact cggaagcag agaagatgaa 1860
gacatgcgta ggagaagtga gaaacatagg agattcatga atatgaaacg tggcttttctt 1920
aacatttag                                     1929
  
```

<210> 4
 <211> 642
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4

```

Met Arg Phe Asp Asp Pro Met Asp Glu Phe Lys Arg Asn Arg Lys Met
  1             5             10             15

Glu Glu Asp Ser Lys Lys Val Ile Asp Val Lys Val Ala Glu Ser Asp
      20             25             30

Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
      35             40             45

Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
      50             55             60
  
```

Asn	Asn	Pro	Phe	Glu	His	Val	Leu	Leu	Glu	Lys	Ser	Glu	Asp	Gly	Leu	
65					70					75					80	
Arg	Phe	Ile	His	Pro	Leu	Glu	Glu	Leu	Ser	Val	Met	Asp	Phe	Val	Asp	
				85					90					95		
Arg	Asn	Leu	Ser	Glu	Met	Arg	Pro	Val	Lys	Pro	Leu	Pro	Leu	Glu	Glu	
			100					105					110			
Thr	Pro	Phe	Lys	Leu	Val	Glu	Glu	Val	Lys	Asp	Leu	Glu	Asp	Leu	Ala	
		115					120					125				
Ala	Ala	Leu	Gln	Ser	Val	Glu	Glu	Phe	Ala	Val	Asp	Leu	Glu	His	Asn	
	130					135					140					
Gln	Tyr	Arg	Thr	Phe	Gln	Gly	Leu	Thr	Cys	Leu	Met	Gln	Ile	Ser	Thr	
145					150					155					160	
Arg	Thr	Glu	Asp	Tyr	Ile	Val	Asp	Ile	Phe	Lys	Leu	Trp	Asp	His	Ile	
				165					170					175		
Gly	Pro	Tyr	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Pro	Lys	Lys	Lys	Lys	Val	
			180					185					190			
Ile	His	Gly	Ala	Asp	Arg	Asp	Ile	Ile	Trp	Leu	Gln	Arg	Asp	Phe	Gly	
		195					200					205				
Ile	Tyr	Val	Cys	Asn	Leu	Phe	Asp	Thr	Gly	Gln	Ala	Ser	Arg	Val	Leu	
	210					215					220					
Lys	Leu	Glu	Arg	Asn	Ser	Leu	Glu	Phe	Leu	Leu	Lys	His	Tyr	Cys	Gly	
225					230					235					240	
Val	Ala	Ala	Asn	Lys	Glu	Tyr	Gln	Lys	Ala	Asp	Trp	Arg	Ile	Arg	Pro	
			245						250					255		
Leu	Pro	Asp	Val	Met	Lys	Arg	Tyr	Ala	Arg	Glu	Asp	Thr	His	Tyr	Leu	
			260					265					270			
Leu	Tyr	Ile	Tyr	Asp	Val	Met	Arg	Met	Glu	Leu	His	Thr	Met	Ala	Lys	
		275					280					285				
Glu	Asp	Glu	Gln	Ser	Asp	Ser	Pro	Leu	Val	Glu	Val	Tyr	Lys	Arg	Ser	
	290					295					300					
Tyr	Asp	Val	Cys	Met	Gln	Leu	Tyr	Glu	Lys	Glu	Leu	Trp	Thr	Arg	Asp	
305					310					315					320	
Ser	Tyr	Leu	His	Val	Tyr	Gly	Val	Gln	Thr	Gly	Asn	Leu	Asn	Ala	Val	
				325					330					335		
Gln	Leu	Ser	Ile	Val	Ala	Leu	Gln	Gly	Leu	Cys	Glu	Trp	Arg	Asp	Arg	
			340					345					350			
Ile	Ala	Arg	Ala	Asp	Asp	Glu	Ser	Thr	Gly	Tyr	Val	Leu	Pro	Asn	Lys	
		355					360					365				

Thr Leu Phe Asp Ile Ala Lys Glu Met Pro Ile Val Val Ala Gln Leu
 370 375 380
 Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
 385 390 395 400
 Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
 405 410 415
 Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
 420 425 430
 Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
 435 440 445
 Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
 450 455 460
 Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
 465 470 475 480
 Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
 485 490 495
 Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
 500 505 510
 Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
 515 520 525
 Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
 530 535 540
 Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
 545 550 555 560
 Asp Asp Asp Asp Asp Asp Asp Glu Ser Tyr Glu Gln Ser Thr Lys Ala
 565 570 575
 Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
 580 585 590
 Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
 595 600 605
 Asp Asp Asp Asp Asp Ser Glu Ser Arg Glu Asp Glu Asp Met Arg Arg
 610 615 620
 Arg Ser Glu Lys His Arg Arg Phe Met Asn Met Lys Arg Gly Phe Leu
 625 630 635 640
 Asn Ile

<210> 5

<211> 714
 <212> DNA
 <213> Arabidopsis thaliana

<400> 5
 atgaatttgc attttgattt ttggtgtttt atatttgaaa ctaatgcaga gaaaccttcg 60
 aatgggtcatc catatgaaac tgagatcact gttttgttag agaatcctca gattgagttt 120
 ggatttttga gaggagagtg ttcatgggaa atgagtgatt catatgtgtg ggttgagaca 180
 gagtcgcagt taaaggaact tgcagaaaata ttagcaaaaag aacaagtttt tgcggttgac 240
 actgagcagc atagtttgcg gtcgtttctt ggtttcactg ctctaattca gatttctaca 300
 catgaggaag acttttttgt ggacacaatt gcgttacatg atgtaatgag tattcttcgt 360
 cctgttttct ctgatacctaa tatttgtaag gtgtttcacg gggctgacaa cgatgttatc 420
 tggcttcaaa gagacttcca tatatatgtt gttaatatgt ttgatactgc caaggcatgt 480
 gaagtgttgt caaagcctca acgatcactg gcatacttac ttgagacagt atgtggagtg 540
 gctactaaca aattgctgca gcgtgaagat tggagacagc gtcctctgtc cgaagagatg 600
 gtgcgatatg ctagaacaga tgcacactat ctgctttata ttgcagatag tttgacaact 660
 gaactcaaac aattagccac tggtaggcat ctttgctatg gagaaacatt ttag 714

<210> 6
 <211> 237
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
 Met Asn Leu His Phe Asp Phe Trp Cys Phe Ile Phe Glu Thr Asn Ala
 1 5 10 15
 Glu Lys Pro Ser Asn Gly His Pro Tyr Glu Thr Glu Ile Thr Val Leu
 20 25 30
 Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
 35 40 45
 Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
 50 55 60
 Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
 65 70 75 80
 Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
 85 90 95
 Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
 100 105 110
 His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
 115 120 125
 Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
 130 135 140
 Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
 145 150 155 160
 Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
 165 170 175

Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
180 185 190

Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala
195 200 205

His Tyr Leu Leu Tyr Ile Ala Asp Ser Leu Thr Thr Glu Leu Lys Gln
210 215 220

Leu Ala Thr Gly Arg His Leu Cys Tyr Gly Glu Thr Phe
225 230 235

<210> 7
<211> 849
<212> DNA
<213> Arabidopsis thaliana

<400> 7
atgcagattg cattctctaa tgcaatatac ttggttgatg tcatcgaagg tggagaggtg 60
attatgaaag cgtgtaagcc tgcactcgag tctaattaca tcacgaaagt tattcacgat 120
tgcaagcgtg acagtgaggc tctatacttc cagtttgagg taagattgca caatgttgtg 180
gacactcaga ttgcttattc tctgattgaa gaacaagaag ggcggaggag acctctagat 240
gattacatat cgtttgtttc actccttgct gatccacgtt actgcggtat atcctatgaa 300
gagaaagaag aagttcgagt tctcatgcgc caggacccaa agttttggac atacaggcct 360
atgactgagc tcatgatccg cgcagctgct gatgatgtcc gcttccttct gtatctctat 420
cacaaaatga tgggaaagct aaatcagcgg tcactatggc atcttgagc tcgtgggtgct 480
ttgtactgtc ggtgtctctg ctgcatgaat gatgctgatt ttgctgattg gccaaaccgtt 540
cctccaattc cagttttcct cgtaaaggtc gtatatgctg tagagacaaa gaaaaaaga 600
cgggtgacat tagcttcgat tgggttactg attgtagttg gactttttaa tgtggcagat 660
aacctgaagt cagaagatca atgtcttgaa gaagagatcc tgtcagtgct tgatgttcca 720
ccaggaaaga tgggacgtgt gattggaagg aaaggagcat cgatcctcgc cattaaggaa 780
gcttgcaacg cggaaattct aattggaggg gcaaagggtc cacctgataa ggtagtctt 840
attccatag 849

<210> 8
<211> 282
<212> PRT
<213> Arabidopsis thaliana

<400> 8
Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
1 5 10 15

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
20 25 30

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
35 40 45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
50 55 60

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
65 70 75 80

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
 85 90 95
 Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
 100 105 110
 Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
 115 120 125
 Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
 130 135 140
 Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
 145 150 155 160
 Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
 165 170 175
 Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
 180 185 190
 Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
 195 200 205
 Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
 210 215 220
 Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
 225 230 235 240
 Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
 245 250 255
 Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
 260 265 270
 Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
 275 280

<210> 9
 <211> 720
 <212> DNA
 <213> Arabidopsis thaliana

<400> 9
 atggctagga tcagaagaag aatccaaaag cgccatatcc acgaaaaccg-ctacatcgat 60
 ttcttttgag aacgtttgat cgtcacggtc actcatacta cctcaaccat ccgccgttgg 120
 attcatagca tccgtttctt cagccgtctt cgctcctcac accctctcgt tgttggaactc 180
 gacgtccaat ggacaccggg tggttccgat cctccaccgg atattctcca actatgtgtt 240
 ggtaaccgct gtctcatcat ccagttgtct cactgtaaag gcattcctga ggtccttcga 300
 agtttcttgg aagatgagac aatcactttt gtcggcgtct ggaacagcca agaccagggc 360
 aagctcgaaa gattccgcca tcagttggag atatggagac ttctagacat aaggcactat 420
 ctgcctacga ggctcctcaa tagttcgttt gagaagattg tagaggagtg tttgggggtac 480
 aagggagtga ggaaagataa ggagatatgt atgagtaatt ggggtgctcg tagcctttcc 540
 catgatcaga ttgttcaggc gtcagatgat gtctatgttt gctgcaagct cgggtgttaag 600

gaatgtatct ggaaagagcg ctcgaatgtt aaagaacgta tctggaaaga gagctcgaat 660
 gttaaggaac atatctggaa agagagctcg aaactttatt ttgttggggg atgtttctga 720

<210> 10
 <211> 239
 <212> PRT
 <213> Arabidopsis thaliana

<400> 10
 Met Ala Arg Ile Arg Arg Arg Ile Gln Lys Arg His Ile His Glu Asn
 1 5 10 15
 Arg Tyr Ile Asp Phe Phe Gly Glu Arg Leu Ile Val Thr Val Thr His
 20 25 30
 Thr Thr Ser Thr Ile Arg Arg Trp Ile His Ser Ile Arg Phe Phe Ser
 35 40 45
 Arg Leu Arg Ser Ser His Pro Leu Val Val Gly Leu Asp Val Gln Trp
 50 55 60
 Thr Pro Gly Gly Ser Asp Pro Pro Pro Asp Ile Leu Gln Leu Cys Val
 65 70 75 80
 Gly Asn Arg Cys Leu Ile Ile Gln Leu Ser His Cys Lys Arg Ile Pro
 85 90 95
 Glu Val Leu Arg Ser Phe Leu Glu Asp Glu Thr Ile Thr Phe Val Gly
 100 105 110
 Val Trp Asn Ser Gln Asp Gln Gly Lys Leu Glu Arg Phe Arg His Gln
 115 120 125
 Leu Glu Ile Trp Arg Leu Leu Asp Ile Arg His Tyr Leu Pro Thr Arg
 130 135 140
 Leu Leu Asn Ser Ser Phe Glu Lys Ile Val Glu Glu Cys Leu Gly Tyr
 145 150 155 160
 Lys Gly Val Arg Lys Asp Lys Glu Ile Cys Met Ser Asn Trp Gly Ala
 165 170 175
 Arg Ser Leu Ser His Asp Gln Ile Val Gln Ala Ser Asp Asp Val Tyr
 180 185 190
 Val Cys Cys Lys Leu Gly Val Lys Glu Cys Ile Trp Lys Glu Arg Ser
 195 200 205
 Asn Val Lys Glu Arg Ile Trp Lys Glu Ser Ser Asn Val Lys Glu His
 210 215 220
 Ile Trp Lys Glu Ser Ser Lys Leu Tyr Phe Val Gly Val Cys Phe
 225 230 235

<210> 11

<211> 654
 <212> DNA
 <213> Arabidopsis thaliana

<400> 11
 atgaagagag gtatcaaaca tctatgtttc aatggcttca cgggctactc atcacttcat 60
 catcattatc atgaacacca cgtcgacttc tttggagaac gtttgatcgt cacagtcact 120
 catactccct cagtgatacg tcgatggatc cacagtatcc gcttcgtcag ccgtcttcgc 180
 ttatcacacc ctctagttgt cggacttggc gttcaatgga cccccgtgg ttccgatacct 240
 ccaccggata ttctccaact atgtgttggg actcgtctgc tcatcattca gttgtctcac 300
 tgtaagtacg tccccgacgt ccttagaagt ttcttgaag atcagacaat cacttttgtc 360
 ggcgtatgga acagccaaga caaggacaag ctcgagagat tccaccatca gttggatatc 420
 tggagacttg tccacataag gcactatctc catccgttgc tcttgagtag ctcgtttgag 480
 acgattgtga aggtgtattt ggggcatgaa ggagtgacga aagataagga gttatgtatg 540
 agtaattggg gtgctcgtag cctctctcat gatcagatag tacaagcgtc acatgatgtc 600
 tatgtttgct gcaagctcgg tgtaaggaa cgtctctgga aaatgggagc ttaa 654

<210> 12
 <211> 217
 <212> PRT
 <213> Arabidopsis thaliana

<400> 12
 Met Lys Arg Gly Ile Lys His Leu Cys Phe Asn Gly Phe Thr Gly Tyr
 1 5 10 15
 Ser Ser Leu His His His Tyr His Glu His His Val Asp Phe Phe Gly
 20 25 30
 Glu Arg Leu Ile Val Thr Val Thr His Thr Pro Ser Val Ile Arg Arg
 35 40 45
 Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
 50 55 60
 Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
 65 70 75 80
 Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
 85 90 95
 Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
 100 105 110
 Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
 115 120 125
 Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
 130 135 140
 His Ile Arg His Tyr Leu His Pro Leu Leu Leu Ser Ser Ser Phe Glu
 145 150 155 160
 Thr Ile Val Lys Val Tyr Leu Gly His Glu Gly Val Thr Lys Asp Lys
 165 170 175

Glu Leu Cys Met Ser Asn Trp Gly Ala Arg Ser Leu Ser His Asp Gln
 180 185 190

Ile Val Gln Ala Ser His Asp Val Tyr Val Cys Cys Lys Leu Gly Val
 195 200 205

Lys Glu Arg Leu Trp Lys Met Gly Ala
 210 215

<210> 13
 <211> 261
 <212> DNA
 <213> Arabidopsis thaliana

<400> 13
 atgatcaagt cgatcgagag ctttattgct cgttatgttt tccaagctac attatacaca 60
 atctggtgcg aacgaaatgg cagaaggcat ggagagagag aggccgaacc agccgctctt 120
 ctaataaaat tgattgataa gcaagccatc tttcctcaat cagagcaact gatgatctac 180
 gctatgacaa gagcctccaa atctggtttg catcgagtgg ttgaaatcaa accatctata 240
 gttcatgtgt ttaaccttta a 261

<210> 14
 <211> 86
 <212> PRT
 <213> Arabidopsis thaliana

<400> 14
 Met Ile Lys Ser Ile Glu Ser Phe Ile Ala Arg Tyr Val Phe Gln Ala
 1 5 10 15
 Thr Leu Tyr Thr Ile Trp Cys Glu Arg Asn Gly Arg Arg His Gly Glu
 20 25 30
 Arg Glu Ala Glu Pro Ala Ala Leu Leu Ile Lys Leu Ile Asp Lys Gln
 35 40 45
 Ala Ile Phe Pro Gln Ser Glu Gln Leu Met Ile Tyr Ala Met Thr Arg
 50 55 60
 Ala Ser Lys Ser Gly Leu His Arg Val Val Glu Ile Lys Pro Ser Ile
 65 70 75 80
 Val His Val Phe Asn Leu
 85

<210> 15
 <211> 2733
 <212> DNA
 <213> C. elegans

<400> 15
 atggaagaag aaccgtacaa aagaaagcta acgaaagccg agaaaaaggc aaaatatcga 60
 acagactacg ccgaaccgtt gaagtcacgc cggaagttc tgaaagcaat tatgaatgga 120
 cccgagtctg agcgggagag aaaagttcga gccaaaaatc gagaattttt caacgaggac 180

tatagatcag	gagtcaacat	ctacggaatg	gctgtggata	tgatgaaagc	gatgccggat	240
agaggaaaaa	catcgggaca	aagtttggcg	gtttggtatc	tggaggattt	tggagtttgg	300
ttaaaagagt	cgggacagga	gacggagctc	agacagaaat	atctgactgg	aactattcaa	360
ataaacgcct	tagatgtgtg	cacaattgga	caaaagcagc	ttctcagtga	aatcttcgat	420
atcaccaaag	agaaattcac	tgaggacatt	acacagttgc	tagatgctgc	catcaagaaa	480
caagacttct	ccgttgctgc	agatatggct	attcagtaca	atcttctacg	ggatcatcat	540
ttcgaacatc	ttgttcttcc	attaatgcta	tctggcaaaag	atcaaacggc	ttataaattg	600
ataagtaaca	atgagaggat	gcaacagcag	cttgtagagt	tttttgatcg	aatggttgga	660
atctcagtgg	ttgccgttga	agagatgctg	aaacctaca	aggaaaccaa	aattatgacg	720
attcctatgg	agaaattgac	gggaaaaacg	ttggacaaac	tcatttctgac	gattatcaac	780
aaaaatactc	acgaatacaa	cttctccagg	gaattgtcga	agttcgccaa	aaaccactca	840
cagaatggga	atctgaaggc	attgaagttt	aatatcagtg	aacgatacga	gaagggaaaa	900
tccgatgaca	actatttcca	gcataatggtt	gaaactttta	ccaaagccga	agatgttcgt	960
gaacctattt	tgttttactt	gtggagctca	aatgcacacc	agaaacaaat	agatgccatc	1020
tgcttttgcta	tctacttagg	aatcgctagt	tccagcagct	atcaactgcc	gaatggttatg	1080
agggacttct	tctgacaacc	tgattcgaag	ctcagagaag	caaaagaact	tctagtgaga	1140
agaaaaacac	tgcaagttcc	tctaaatggc	gaacaattat	tcgtatttga	gaatgagcga	1200
agaactcaaa	tccacatggg	gaaaactgaa	tctgagatga	attacttatg	ttccgagatc	1260
aaatcactaa	gcgacgagcc	agcacctgtt	tacgttggat	tcgattctga	gtggaaaaccg	1320
tcgaatctta	cagctgttca	tgactcgaaa	attgctatca	tacaattggt	cttcaaaaaat	1380
tgtgtatggc	ttgtggattg	cgtagaatta	gaaaaggcaa	atatggcaga	tgactggtgg	1440
caaaagttcg	catctcgatt	gttcggagat	tctcctgtaa	aagtcgtagg	atttgatatg	1500
aggaacgatc	tggatgcaat	ggctacaatc	ccagcactga	agtcatccat	gaagatagaa	1560
gataccaaaa	atgcattcga	tctgaagcga	ttagcagaga	atgtttgcga	tatcgacatg	1620
gaaatttttag	agctgccaaa	gaagactttc	aaattggcag	atttgacaca	ttatctactg	1680
ggattggagc	tcgacaaaac	tgaacaatgc	agtaactggc	aatgtcgtcc	tctgcgaaaa	1740
aaacaaattg	tgtacgcagc	attggacgca	gttgtcgtgg	tggaacatt	caagaaaatc	1800
ttgtcgattg	tagaggagaa	aaacaaggac	gcagatatcg	agaagattgt	cagagaatca	1860
aatgtaattg	ctccgaaaaa	agacaaagga	cacaaatcgt	accgcaagct	gaaaactatt	1920
ccatggcttg	agctctacga	tatcttgcca	agccatcgta	atcctacgag	atcaccacag	1980
cgaccacacg	acattaaagt	tattgttgac	acaatgctga	ttggatttgg	aaagaatctg	2040
aggagagttg	gaattgatgt	tattcttcca	aaagacgtga	gcgacttccg	aaagtacctg	2100
aaggaaattg	aacgagttgg	cggcgagcat	ctacgtcata	taatcacagt	gccatcgaaa	2160
agttacgaag	ccttgaaaaa	ggattatgat	aattatacaa	ttgcaattcc	ggaactcaat	2220
aacatgtctc	ccgtagatca	gcttattgag	tttttcgacc	tggtcaacgt	agatattcgt	2280
ccggaagacg	tatatcctcg	atgcactgaa	tgcaattctc	ggcttcaaat	taaattcccc	2340
ggaccagttt	tacatttctt	gcaccaatac	tgtgtcatcc	atgtgcaaaa	tgtttatcgt	2400
gcggatatga	gcgaatttcc	actggaagaa	tggtggaatc	gtatgcttca	tatcaatcca	2460
gacgactacg	acggagtaaa	agtggaaatg	tcgcgaccat	ctccaacaag	caagtggatc	2520
gtggcaactg	ttcccacagg	atgcctacat	attacgcgac	aaactgcact	tcacaccaat	2580
ctgccagatg	gaattgaagt	tcgaatccac	aaagtgcctg	atgacgagtt	caagcgtcga	2640
aatctcagct	tctatgtgtg	tggagaatgc	ggtacgggtg	cttgtgatgg	tcgtggcaat	2700
caagcgtcgg	agagcaccag	ccaggaatgt	tga			2733

<210> 16
 <211> 910
 <212> PRT
 <213> C. elegans

<400> 16
 Met Glu Glu Glu Pro Tyr Lys Arg Lys Leu Thr Lys Ala Glu Lys Lys
 1 5 10 15
 Ala Lys Tyr Arg Thr Asp Tyr Ala Glu Pro Leu Lys Ser Arg Arg Glu
 20 25 30

Val	Leu	Lys	Ala	Ile	Met	Asn	Gly	Pro	Glu	Ser	Glu	Arg	Glu	Arg	Lys	
		35					40					45				
Val	Arg	Ala	Lys	Asn	Arg	Glu	Phe	Phe	Asn	Glu	Asp	Tyr	Arg	Ser	Gly	
	50					55					60					
Val	Asn	Ile	Tyr	Gly	Met	Ala	Val	Asp	Met	Met	Lys	Ala	Met	Pro	Asp	
	65				70					75					80	
Arg	Gly	Lys	Thr	Ser	Gly	Gln	Ser	Leu	Ala	Val	Trp	Tyr	Leu	Glu	Asp	
				85					90					95		
Phe	Gly	Val	Trp	Leu	Lys	Glu	Ser	Gly	Gln	Glu	Thr	Glu	Leu	Arg	Gln	
			100					105					110			
Lys	Tyr	Leu	Thr	Gly	Thr	Ile	Gln	Ile	Asn	Ala	Leu	Asp	Val	Cys	Thr	
		115					120					125				
Ile	Gly	Gln	Lys	Gln	Leu	Leu	Ser	Glu	Ile	Phe	Asp	Ile	Thr	Lys	Glu	
	130					135					140					
Lys	Phe	Thr	Glu	Asp	Ile	Thr	Gln	Leu	Leu	Asp	Ala	Ala	Ile	Lys	Lys	
	145				150					155					160	
Gln	Asp	Phe	Ser	Val	Ala	Ala	Asp	Met	Ala	Ile	Gln	Tyr	Asn	Leu	Leu	
				165					170					175		
Arg	Asp	His	His	Phe	Glu	His	Leu	Val	Leu	Pro	Leu	Met	Leu	Ser	Gly	
			180					185					190			
Lys	Asp	Gln	Thr	Ala	Tyr	Lys	Leu	Ile	Ser	Asn	Asn	Glu	Arg	Met	Gln	
		195					200					205				
Gln	Gln	Leu	Val	Glu	Phe	Phe	Asp	Arg	Met	Val	Gly	Ile	Ser	Val	Val	
	210					215					220					
Ala	Val	Glu	Glu	Met	Leu	Lys	Pro	Tyr	Lys	Glu	Thr	Lys	Ile	Met	Thr	
	225				230					235					240	
Ile	Pro	Met	Glu	Lys	Leu	Thr	Gly	Lys	Thr	Leu	Asp	Lys	Leu	Ile	Ser	
				245					250					255		
Thr	Ile	Ile	Asn	Lys	Asn	Thr	His	Glu	Tyr	Asn	Phe	Ser	Arg	Glu	Leu	
			260					265					270			
Ser	Lys	Phe	Ala	Lys	Asn	His	Ser	Gln	Asn	Gly	Asn	Leu	Lys	Ala	Leu	
		275					280					285				
Lys	Phe	Asn	Ile	Ser	Glu	Arg	Tyr	Glu	Lys	Gly	Lys	Ser	Asp	Asp	Asn	
	290					295					300					
Tyr	Phe	Gln	His	Met	Val	Glu	Thr	Phe	Thr	Lys	Ala	Glu	Asp	Val	Arg	
	305				310					315					320	
Glu	Pro	Ile	Leu	Phe	Tyr	Leu	Trp	Ser	Ser	Asn	Asp	Thr	Glu	Lys	Gln	
				325					330					335		

Ile	Asp	Ala	Ile	Cys	Phe	Ala	Ile	Tyr	Leu	Gly	Ile	Ala	Ser	Ser	Ser		
			340					345					350				
Ser	Tyr	Gln	Leu	Pro	Asn	Val	Met	Arg	Asp	Phe	Phe	Arg	Gln	Pro	Asp		
		355					360					365					
Ser	Lys	Leu	Arg	Glu	Ala	Lys	Glu	Leu	Leu	Val	Arg	Arg	Lys	Thr	Leu		
	370					375					380						
Gln	Val	Pro	Leu	Asn	Gly	Glu	Gln	Leu	Phe	Val	Phe	Glu	Asn	Glu	Arg		
385					390					395					400		
Arg	Thr	Gln	Ile	His	Met	Val	Lys	Thr	Glu	Ser	Glu	Met	Asn	Tyr	Leu		
				405					410					415			
Cys	Ser	Glu	Ile	Lys	Ser	Leu	Ser	Asp	Glu	Pro	Ala	Pro	Val	Tyr	Val		
			420					425					430				
Gly	Phe	Asp	Ser	Glu	Trp	Lys	Pro	Ser	Asn	Leu	Thr	Ala	Val	His	Asp		
		435					440					445					
Ser	Lys	Ile	Ala	Ile	Ile	Gln	Leu	Phe	Phe	Lys	Asn	Cys	Val	Trp	Leu		
	450					455					460						
Val	Asp	Cys	Val	Glu	Leu	Glu	Lys	Ala	Asn	Met	Ala	Asp	Asp	Trp	Trp		
465					470					475					480		
Gln	Lys	Phe	Ala	Ser	Arg	Leu	Phe	Gly	Asp	Ser	Pro	Val	Lys	Val	Val		
				485					490					495			
Gly	Phe	Asp	Met	Arg	Asn	Asp	Leu	Asp	Ala	Met	Ala	Thr	Ile	Pro	Ala		
			500					505					510				
Leu	Lys	Ser	Ser	Met	Lys	Ile	Glu	Asp	Thr	Lys	Asn	Ala	Phe	Asp	Leu		
		515					520					525					
Lys	Arg	Leu	Ala	Glu	Asn	Val	Cys	Asp	Ile	Asp	Met	Glu	Ile	Leu	Glu		
	530					535					540						
Leu	Pro	Lys	Lys	Thr	Phe	Lys	Leu	Ala	Asp	Leu	Thr	His	Tyr	Leu	Leu		
545					550					555					560		
Gly	Leu	Glu	Leu	Asp	Lys	Thr	Glu	Gln	Cys	Ser	Asn	Trp	Gln	Cys	Arg		
				565					570					575			
Pro	Leu	Arg	Lys	Lys	Gln	Ile	Val	Tyr	Ala	Ala	Leu	Asp	Ala	Val	Val		
			580					585					590				
Val	Val	Glu	Thr	Phe	Lys	Lys	Ile	Leu	Ser	Ile	Val	Glu	Glu	Lys	Asn		
		595					600					605					
Lys	Asp	Ala	Asp	Ile	Glu	Lys	Ile	Val	Arg	Glu	Ser	Asn	Val	Met	Ala		
	610					615					620						
Pro	Lys	Lys	Asp	Lys	Gly	His	Lys	Ser	Tyr	Arg	Lys	Leu	Lys	Thr	Ile		
625					630					635					640		

Pro Trp Leu Glu Leu Tyr Asp Ile Leu Arg Ser His Arg Asn Pro Thr
 645 650 655
 Arg Ser Pro Gln Arg Pro His Asp Ile Lys Val Ile Val Asp Thr Met
 660 665 670
 Leu Ile Gly Phe Gly Lys Asn Leu Arg Arg Val Gly Ile Asp Val Ile
 675 680 685
 Leu Pro Lys Asp Val Ser Asp Phe Arg Lys Tyr Leu Lys Glu Ile Glu
 690 695 700
 Arg Val Gly Gly Glu His Leu Arg His Ile Ile Thr Val Pro Ser Lys
 705 710 715 720
 Ser Tyr Glu Ala Leu Lys Met Asp Tyr Asp Asn Tyr Thr Ile Ala Ile
 725 730 735
 Pro Glu Leu Asn Asn Met Ser Pro Val Asp Gln Leu Ile Glu Phe Phe
 740 745 750
 Asp Leu Phe Asn Val Asp Ile Arg Pro Glu Asp Val Tyr Pro Arg Cys
 755 760 765
 Thr Glu Cys Asn Ser Arg Leu Gln Ile Lys Phe Pro Gly Pro Val Leu
 770 775 780
 His Phe Leu His Gln Tyr Cys Val Ile His Val Gln Asn Val Tyr Arg
 785 790 795 800
 Ala Asp Met Ser Glu Phe Pro Leu Glu Glu Trp Trp Asn Arg Met Leu
 805 810 815
 His Ile Asn Pro Asp Asp Tyr Asp Gly Val Lys Val Glu Met Ser Arg
 820 825 830
 Pro Ser Pro Thr Ser Lys Trp Ile Val Ala Thr Val Pro Thr Gly Cys
 835 840 845
 Leu His Ile Thr Arg Gln Thr Ala Leu His Thr Asn Leu Pro Asp Gly
 850 855 860
 Ile Glu Val Arg Ile His Lys Val Pro Asp Asp Glu Phe Lys Arg Arg
 865 870 875 880
 Asn Leu Ser Phe Tyr Val Cys Gly Glu Cys Gly Thr Val Ala Cys Asp
 885 890 895
 Gly Arg Gly Asn Gln Ala Ser Glu Ser Thr Ser Gln Glu Cys
 900 905 910

<210> 17
 <211> 4299
 <212> DNA
 <213> Homo sapiens

<400> 17

atgagtga	aaaaattgga	aacaactgca	cagcagcgga	aatgtcctga	atggatgaat	60
gtgcagaata	aaagatgtgc	tgtagaagaa	agaaaggcat	gtgttcggaa	gagtgttttt	120
gaagatgacc	tccccttctt	agaattcact	ggatccattg	tgtatagtta	cgatgctagt	180
gattgtctct	tcctgtcaga	agatattagc	atgagtctat	cagatgggga	tgtgggtggga	240
tttgacatgg	agtggccacc	attatacaat	agagggaac	ttggcaaagt	tgcactaatt	300
cagttgtgtg	tttctgagag	caaatgttac	ttgttccacg	tttcttccat	gtcagttttt	360
ccccagggat	taaaaatggt	gcttgaaaat	aaagcagtta	aaaaggcagg	tgtaggaatt	420
gaaggagatc	agtggaaact	tctacgtgac	tttgatatca	aattgaagaa	ttttgtggag	480
ttgacagatg	ttgccaataa	aaagctgaaa	tgtacagaga	cctggagcct	taacagtctg	540
gttaaaccac	tcttaggtaa	acagctcctg	aaagacaagt	ctatccgctg	tagcaattgg	600
agtaaatttc	ctctcactga	ggaccagaaa	ctgtatgcag	ccactgatgc	ttatgctggg	660
tttattattt	accgaaattt	agagattttg	gatgatactg	tgcaaagggt	tgctataaat	720
aaagaggaag	aaatcctact	tagcgacatg	aacaaacagt	tgacttcaat	ctctgaggaa	780
gtgatggatc	tggctaagca	tcttcctcat	gctttcagta	aattggaaaa	cccacggagg	840
gtttctatct	tactaaagga	tatttcagaa	aatctatatt	cactgaggag	gatgataatt	900
gggtctacta	acattgagac	tgaactgagg	cccagcaata	atttaaactt	attatccttt	960
gaagattcaa	ctactggggg	agtacaacag	aaacaaatta	gagaacatga	agttttaatt	1020
cacgttgaag	atgaaacatg	ggacccaaca	cttgatcatt	tagctaaaca	tgatggagaa	1080
gatgtacttg	gaaataaagt	ggaacgaaaa	gaagatggat	ttgaagatgg	agtagaagac	1140
aacaaattga	aagagaatat	ggaaagagct	tgtttgatgt	cgttagatat	tacagaacat	1200
gaactccaaa	ttttggaaca	gcagtctcag	gaagaatatc	ttagtgatat	tgcttataaa	1260
tctactgagc	atttatctcc	caatgataat	gaaaacgata	cgtcctatgt	aattgagagt	1320
gatgaagatt	tagaaatgga	gatgcttaag	catttatctc	ccaatgataa	tgaaaacgat	1380
acgtcctatg	taattgagag	tgatgaagat	ttagaaatgg	agatgcttaa	gtcttttagaa	1440
aacctcaata	gtggcacggg	agaaccaact	cattctaaat	gcttaaaaa	ggaaagaaat	1500
ctgggtcttc	ctactaaaga	agaagaagaa	gatgatgaaa	atgaagctaa	tgaaggggaa	1560
gaagatgatg	ataaggactt	tttgtggcca	gcacccaatg	aagagcaagt	tacttgccctc	1620
aagatgtact	ttggccattc	cagtttttaa	ccagttcagt	ggaaagtgat	tcattcagta	1680
ttagaagaaa	gaagagataa	tgttgctgtc	atggcaactg	gatatggaaa	gagtttgtgc	1740
ttccagtatc	cacctgttta	tgtaggcaag	attggccttg	ttatctctcc	ccttattttc	1800
ctgatggaag	accaagtgtc	acagcttaaa	atgtccaaca	tcccagcttg	cttccttgga	1860
tcagcacagc	cagaaaatgt	tctaacagat	attaaattag	gtaaataccg	gattgtatac	1920
gtaactccag	aatactgttc	aggtaacatg	ggcctgctcc	agcaacttga	ggctgatatt	1980
ggtatcacgc	tcattgtgtg	ggatgaggct	cactgtattt	ctgagtgggg	gcatgatatt	2040
agggatccat	tcaggaagtt	gggtccctta	aagacagcac	tgccaatggt	tccaatcggt	2100
gcacttactg	ctactgcaag	ttcttcaatc	cgggaagaca	ttgtacgttg	cttaaatctg	2160
agaaatcctc	agatcacctg	tactggtttt	gatcgaccaa	acctgtattt	agaagttagg	2220
cgaaaaacag	ggaatatcct	tcaggatctg	cagccatttc	ttgtcaaaac	aagttcccac	2280
tggaattttg	aaggtccaac	aatcatctac	tgtccttcta	gaaaaatgac	acaacaagtt	2340
acaggtgaac	ttaggaaact	taatctatcc	tgtggaacat	accatgcggg	catgagtttt	2400
agcacaagga	aagacattca	tcataggttt	gtaagagatg	aaattcagtg	tgtcatagct	2460
accatagctt	ttggaatggg	cattaataaa	gctgacattc	gccaagtcac	tcattacggg	2520
gctcctaagg	acatggaatc	atattatcag	gagattggta	gagctgggtc	tgatggactt	2580
caaagttctt	gtcacgtcct	ctgggctcct	gcagacatta	acttaaatag	gcaccttctt	2640
actgagatac	gtaatgagaa	gtttcgatta	tacaaattaa	agatgatggc	aaagatggaa	2700
aaatatcttc	attctagcag	atgtaggaga	caaatcatct	tgtctcattt	tgaggacaaa	2760
caagtacaaa	aagcctcctt	gggaattatg	ggaactgaaa	aatgctgtga	taattgcagg	2820
tccagattgg	atcattgcta	ttccatggat	gactcagagg	atacatcctg	ggactttggg	2880
ccacaagcat	ttaagctttt	gtctgctgtg	gacatcttag	gcgaaaaatt	tggaattggg	2940
cttccaattt	tattttctcc	aggatctaata	tctcagcgtc	ttgccgatca	atatcgagg	3000
cacagtttat	ttggcactgg	caaggatcaa	acagagagtt	gggtggaagg	tttttccggt	3060
cagctgatca	ctgagggatt	cttggtagaa	gtttctcggt	ataacaaatt	tatgaagatt	3120
tgcgccttta	cgaaaaagg	tagaaattgg	cttcataaa	ctaatacaga	atctcagagc	3180
ctcatccttc	aagctaattga	agaatttgtgt	ccaaagaagt	ttcttctgcc	tagttcgaaa	3240
actgtatctt	cgggcaccaa	agagcattgt	tataatcaag	taccagttga	attaagtaca	3300
gagaagaagt	ctaacttggg	gaagttatat	tcttataaac	catgtgataa	gatttcttct	3360


```

gggagtaaca tttctaaaaa aagtatcatg gtacagtcac cagaaaaagc ttacagttcc 3420
tcacagcctg ttatttcggc acaagagcag gagactcaga ttgtgttata tggcaaattg 3480
gtagaagcta ggcagaaaca tgccaataaa atggatgttc ccccagctat tctggcaaca 3540
aacaagatac tgggtgatat ggccaaaatg agaccaacta cggttgaaaa cgtaaaaagg 3600
attgatggtg tttctgaagg caaagctgcc atgttggccc ctctgttgga agtcatcaaa 3660
catttctgcc aaacaaatag tggtcagaca gacctctttt caagtacaaa acctcaagaa 3720
gaacagaaga cgagtctggt agcaaaaaat aaaatatgca cactttcaca gtctatggcc 3780
atcacatact ctttattcca agaaaagaag atgcctttga agagcatagc tgagagcagg 3840
attctgcctc tcatgacaat tggcatgcac ttatcccaag cggtgaaaagc tggctgcccc 3900
cttgatttgg agcagagcagg cctgactcca gaggttcaga agattattgc tgatgttatc 3960
cgaaaccctc ccgtcaactc agatatgagt aaaattagcc taatcagaat gttagttcct 4020
gaaaacattg acacgtacct tatccacatg gcaattgaga tccttaaaaa tggtcctgac 4080
agcggacttc aaccttcattg tgatgtcaac aaaaggagat gttttcccg tttctgaagag 4140
atctgttcaa gttctaagag aagcaaggaa gaagtaggca tcaatactga gacttcattc 4200
gcagagagaa agagacgatt acctgtgtgg tttgccaaag gaagtgtatc cagcaagaaa 4260
ttaatggaca aaacgaaaag gggaggtcct tttagttaa 4299

```

<210> 18
 <211> 1432
 <212> PRT
 <213> Homo sapiens

```

<400> 18
Met Ser Glu Lys Lys Leu Glu Thr Thr Ala Gln Gln Arg Lys Cys Pro
  1                      5                      10                      15

Glu Trp Met Asn Val Gln Asn Lys Arg Cys Ala Val Glu Glu Arg Lys
          20                      25                      30

Ala Cys Val Arg Lys Ser Val Phe Glu Asp Asp Leu Pro Phe Leu Glu
          35                      40                      45

Phe Thr Gly Ser Ile Val Tyr Ser Tyr Asp Ala Ser Asp Cys Ser Phe
          50                      55                      60

Leu Ser Glu Asp Ile Ser Met Ser Leu Ser Asp Gly Asp Val Val Gly
          65                      70                      75                      80

Phe Asp Met Glu Trp Pro Pro Leu Tyr Asn Arg Gly Lys Leu Gly Lys
          85                      90                      95

Val Ala Leu Ile Gln Leu Cys Val Ser Glu Ser Lys Cys Tyr Leu Phe
          100                      105                      110

His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
          115                      120                      125

Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
          130                      135                      140

Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
          145                      150                      155                      160

Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
          165                      170                      175

```

Leu	Asn	Ser	Leu	Val	Lys	His	Leu	Leu	Gly	Lys	Gln	Leu	Leu	Lys	Asp	180	185	190	
Lys	Ser	Ile	Arg	Cys	Ser	Asn	Trp	Ser	Lys	Phe	Pro	Leu	Thr	Glu	Asp	195	200	205	
Gln	Lys	Leu	Tyr	Ala	Ala	Thr	Asp	Ala	Tyr	Ala	Gly	Phe	Ile	Ile	Tyr	210	215	220	
Arg	Asn	Leu	Glu	Ile	Leu	Asp	Asp	Thr	Val	Gln	Arg	Phe	Ala	Ile	Asn	225	230	235	240
Lys	Glu	Glu	Glu	Ile	Leu	Leu	Ser	Asp	Met	Asn	Lys	Gln	Leu	Thr	Ser	245	250	255	
Ile	Ser	Glu	Glu	Val	Met	Asp	Leu	Ala	Lys	His	Leu	Pro	His	Ala	Phe	260	265	270	
Ser	Lys	Leu	Glu	Asn	Pro	Arg	Arg	Val	Ser	Ile	Leu	Leu	Lys	Asp	Ile	275	280	285	
Ser	Glu	Asn	Leu	Tyr	Ser	Leu	Arg	Arg	Met	Ile	Ile	Gly	Ser	Thr	Asn	290	295	300	
Ile	Glu	Thr	Glu	Leu	Arg	Pro	Ser	Asn	Asn	Leu	Asn	Leu	Leu	Ser	Phe	305	310	315	320
Glu	Asp	Ser	Thr	Thr	Gly	Gly	Val	Gln	Gln	Lys	Gln	Ile	Arg	Glu	His	325	330	335	
Glu	Val	Leu	Ile	His	Val	Glu	Asp	Glu	Thr	Trp	Asp	Pro	Thr	Leu	Asp	340	345	350	
His	Leu	Ala	Lys	His	Asp	Gly	Glu	Asp	Val	Leu	Gly	Asn	Lys	Val	Glu	355	360	365	
Arg	Lys	Glu	Asp	Gly	Phe	Glu	Asp	Gly	Val	Glu	Asp	Asn	Lys	Leu	Lys	370	375	380	
Glu	Asn	Met	Glu	Arg	Ala	Cys	Leu	Met	Ser	Leu	Asp	Ile	Thr	Glu	His	385	390	395	400
Glu	Leu	Gln	Ile	Leu	Glu	Gln	Gln	Ser	Gln	Glu	Glu	Tyr	Leu	Ser	Asp	405	410	415	
Ile	Ala	Tyr	Lys	Ser	Thr	Glu	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn	420	425	430	
Asp	Thr	Ser	Tyr	Val	Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met	435	440	445	
Leu	Lys	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn	Asp	Thr	Ser	Tyr	Val	450	455	460	
Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met	Leu	Lys	Ser	Leu	Glu	465	470	475	480

Asn Leu Asn Ser Gly Thr Val Glu Pro Thr His Ser Lys Cys Leu Lys
 485 490 495
 Met Glu Arg Asn Leu Gly Leu Pro Thr Lys Glu Glu Glu Glu Asp Asp
 500 505 510
 Glu Asn Glu Ala Asn Glu Gly Glu Glu Asp Asp Asp Lys Asp Phe Leu
 515 520 525
 Trp Pro Ala Pro Asn Glu Glu Gln Val Thr Cys Leu Lys Met Tyr Phe
 530 535 540
 Gly His Ser Ser Phe Lys Pro Val Gln Trp Lys Val Ile His Ser Val
 545 550 555 560
 Leu Glu Glu Arg Arg Asp Asn Val Ala Val Met Ala Thr Gly Tyr Gly
 565 570 575
 Lys Ser Leu Cys Phe Gln Tyr Pro Pro Val Tyr Val Gly Lys Ile Gly
 580 585 590
 Leu Val Ile Ser Pro Leu Ile Ser Leu Met Glu Asp Gln Val Leu Gln
 595 600 605
 Leu Lys Met Ser Asn Ile Pro Ala Cys Phe Leu Gly Ser Ala Gln Ser
 610 615 620
 Glu Asn Val Leu Thr Asp Ile Lys Leu Gly Lys Tyr Arg Ile Val Tyr
 625 630 635 640
 Val Thr Pro Glu Tyr Cys Ser Gly Asn Met Gly Leu Leu Gln Gln Leu
 645 650 655
 Glu Ala Asp Ile Gly Ile Thr Leu Ile Ala Val Asp Glu Ala His Cys
 660 665 670
 Ile Ser Glu Trp Gly His Asp Phe Arg Asp Ser Phe Arg Lys Leu Gly
 675 680 685
 Ser Leu Lys Thr Ala Leu Pro Met Val Pro Ile Val Ala Leu Thr Ala
 690 695 700
 Thr Ala Ser Ser Ser Ile Arg Glu Asp Ile Val Arg Cys Leu Asn Leu
 705 710 715 720
 Arg Asn Pro Gln Ile Thr Cys Thr Gly Phe Asp Arg Pro Asn Leu Tyr
 725 730 735
 Leu Glu Val Arg Arg Lys Thr Gly Asn Ile Leu Gln Asp Leu Gln Pro
 740 745 750
 Phe Leu Val Lys Thr Ser Ser His Trp Glu Phe Glu Gly Pro Thr Ile
 755 760 765
 Ile Tyr Cys Pro Ser Arg Lys Met Thr Gln Gln Val Thr Gly Glu Leu
 770 775 780

Arg	Lys	Leu	Asn	Leu	Ser	Cys	Gly	Thr	Tyr	His	Ala	Gly	Met	Ser	Phe	
785					790					795					800	
Ser	Thr	Arg	Lys	Asp	Ile	His	His	Arg	Phe	Val	Arg	Asp	Glu	Ile	Gln	
				805					810					815		
Cys	Val	Ile	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asn	Lys	Ala	Asp	
			820					825					830			
Ile	Arg	Gln	Val	Ile	His	Tyr	Gly	Ala	Pro	Lys	Asp	Met	Glu	Ser	Tyr	
		835					840					845				
Tyr	Gln	Glu	Ile	Gly	Arg	Ala	Gly	Arg	Asp	Gly	Leu	Gln	Ser	Ser	Cys	
	850					855					860					
His	Val	Leu	Trp	Ala	Pro	Ala	Asp	Ile	Asn	Leu	Asn	Arg	His	Leu	Leu	
865					870					875					880	
Thr	Glu	Ile	Arg	Asn	Glu	Lys	Phe	Arg	Leu	Tyr	Lys	Leu	Lys	Met	Met	
				885					890					895		
Ala	Lys	Met	Glu	Lys	Tyr	Leu	His	Ser	Ser	Arg	Cys	Arg	Arg	Gln	Ile	
			900					905						910		
Ile	Leu	Ser	His	Phe	Glu	Asp	Lys	Gln	Val	Gln	Lys	Ala	Ser	Leu	Gly	
		915					920					925				
Ile	Met	Gly	Thr	Glu	Lys	Cys	Cys	Asp	Asn	Cys	Arg	Ser	Arg	Leu	Asp	
	930					935					940					
His	Cys	Tyr	Ser	Met	Asp	Asp	Ser	Glu	Asp	Thr	Ser	Trp	Asp	Phe	Gly	
945					950					955					960	
Pro	Gln	Ala	Phe	Lys	Leu	Leu	Ser	Ala	Val	Asp	Ile	Leu	Gly	Glu	Lys	
				965					970					975		
Phe	Gly	Ile	Gly	Leu	Pro	Ile	Leu	Phe	Leu	Arg	Gly	Ser	Asn	Ser	Gln	
			980					985					990			
Arg	Leu	Ala	Asp	Gln	Tyr	Arg	Arg	His	Ser	Leu	Phe	Gly	Thr	Gly	Lys	
		995					1000					1005				
Asp	Gln	Thr	Glu	Ser	Trp	Trp	Lys	Ala	Phe	Ser	Arg	Gln	Leu	Ile	Thr	
	1010					1015					1020					
Glu	Gly	Phe	Leu	Val	Glu	Val	Ser	Arg	Tyr	Asn	Lys	Phe	Met	Lys	Ile	
1025				1030					1035					1040		
Cys	Ala	Leu	Thr	Lys	Lys	Gly	Arg	Asn	Trp	Leu	His	Lys	Ala	Asn	Thr	
				1045				1050					1055			
Glu	Ser	Gln	Ser	Leu	Ile	Leu	Gln	Ala	Asn	Glu	Glu	Leu	Cys	Pro	Lys	
			1060				1065					1070				
Lys	Phe	Leu	Leu	Pro	Ser	Ser	Lys	Thr	Val	Ser	Ser	Gly	Thr	Lys	Glu	
		1075					1080					1085				

His Cys Tyr Asn Gln Val Pro Val Glu Leu Ser Thr Glu Lys Lys Ser
 1090 1095 1100
 Asn Leu Glu Lys Leu Tyr Ser Tyr Lys Pro Cys Asp Lys Ile Ser Ser
 1105 1110 1115 1120
 Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys
 1125 1130 1135
 Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr
 1140 1145 1150
 Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala
 1155 1160 1165
 Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu
 1170 1175 1180
 Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg
 1185 1190 1195 1200
 Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu
 1205 1210 1215
 Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu
 1220 1225 1230
 Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala
 1235 1240 1245
 Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser
 1250 1255 1260
 Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg
 1265 1270 1275 1280
 Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys
 1285 1290 1295
 Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val
 1300 1305 1310
 Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp
 1315 1320 1325
 Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp
 1330 1335 1340
 Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp
 1345 1350 1355 1360
 Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro
 1365 1370 1375
 Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val
 1380 1385 1390

Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro
 1395 1400 1405

Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys
 1410 1415 1420

Thr Lys Arg Gly Gly Leu Phe Ser
 1425 1430

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220> Misc_feature
 <223> 1...30

<400> 19
 cgacatgatc tgatacatcg ttatgccatt 30

<210> 20
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220> Misc_feature
 <223> 1...29

<400> 20
 cattttataa taacgctgcg gacatctac 29

<210> 21
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

<400> 21
 atgtttgagt ttttcgcttc aggaggaagg tcgccgacac aagaagctaa tgagccacca 60
 gttccgattt acattgtgac ggatccggtt caacttcctg ctgatttcct aaacccttct 120
 cctgaaaaga aattgggttat cggttttgac tgtgaggggtg ttgacctctg ccgacatggg 180
 aaactttgta tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240
 ggtggagagg tgattatgaa agcgtgtaag cctgcactcg agtctaatta catcacgaaa 300
 gttattcacg attgcaagcg tgacagtga gctctatact tccagtttgg gataagattg 360
 cacaatgttg tggacactca gattgcttat tctctgattg aagaacaaga agggcggagg 420
 agacctctag atgattacat atcgtttgtt tcaactcctg ctgatccacg ttactgcggt 480
 atatcctatg aagagaaaaga agaagttcga gttctcatgc gccaggaccc aaagttttgg 540
 acatacaggc ctatgactga gctcatgatc cgcgcagctg ctgatgatgt ccgcttcctt 600
 ctgtatctct atcacaaaat gatgggaaag ctaaatcagc ggtcactatg gcatcttgca 660
 gttcgtgggtg ctttgtactg tcggtgtctc tgctgcatga atgatgctga ttttgctgat 720
 tggccaaccg ttcctccaat tccagttttc ctcggttaagg tcgtatatgc tgtagagaca 780
 aagaaaaaaa gacgggtgac attagcttcg attgggttac tgattgtagt tggactttta 840
 aatgtggcag ataacctgaa gtcagaagat caatgtcttg aagaagagat cctgtcagtg 900
 cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960
 gccattaagg aagcttgcaa cgcggaatt ctaattggag gggcaaaggg tccacctgat 1020

aaggtagtc ttattccata g

1041

<210> 22
 <211> 346
 <212> PRT
 <213> Arabidopsis thaliana

<400> 22

Met	Phe	Glu	Phe	Phe	Ala	Ser	Gly	Gly	Arg	Ser	Pro	Thr	Gln	Glu	Ala	1	5	10	15
Asn	Glu	Pro	Pro	Val	Pro	Ile	Tyr	Ile	Val	Thr	Asp	Pro	Phe	Gln	Leu	20	25	30	
Pro	Ala	Asp	Phe	Leu	Asn	Pro	Ser	Pro	Glu	Lys	Lys	Leu	Val	Ile	Gly	35	40	45	
Phe	Asp	Cys	Glu	Gly	Val	Asp	Leu	Cys	Arg	His	Gly	Lys	Leu	Cys	Ile	50	55	60	
Met	Gln	Ile	Ala	Phe	Ser	Asn	Ala	Ile	Tyr	Leu	Val	Asp	Val	Ile	Glu	65	70	75	80
Gly	Gly	Glu	Val	Ile	Met	Lys	Ala	Cys	Lys	Pro	Ala	Leu	Glu	Ser	Asn	85	90	95	
Tyr	Ile	Thr	Lys	Val	Ile	His	Asp	Cys	Lys	Arg	Asp	Ser	Glu	Ala	Leu	100	105	110	
Tyr	Phe	Gln	Phe	Gly	Ile	Arg	Leu	His	Asn	Val	Val	Asp	Thr	Gln	Ile	115	120	125	
Ala	Tyr	Ser	Leu	Ile	Glu	Glu	Gln	Glu	Gly	Arg	Arg	Arg	Pro	Leu	Asp	130	135	140	
Asp	Tyr	Ile	Ser	Phe	Val	Ser	Leu	Leu	Ala	Asp	Pro	Arg	Tyr	Cys	Gly	145	150	155	160
Ile	Ser	Tyr	Glu	Glu	Lys	Glu	Glu	Val	Arg	Val	Leu	Met	Arg	Gln	Asp	165	170	175	
Pro	Lys	Phe	Trp	Thr	Tyr	Arg	Pro	Met	Thr	Glu	Leu	Met	Ile	Arg	Ala	180	185	190	
Ala	Ala	Asp	Asp	Val	Arg	Phe	Leu	Leu	Tyr	Leu	Tyr	His	Lys	Met	Met	195	200	205	
Gly	Lys	Leu	Asn	Gln	Arg	Ser	Leu	Trp	His	Leu	Ala	Val	Arg	Gly	Ala	210	215	220	
Leu	Tyr	Cys	Arg	Cys	Leu	Cys	Cys	Met	Asn	Asp	Ala	Asp	Phe	Ala	Asp	225	230	235	240
Trp	Pro	Thr	Val	Pro	Pro	Ile	Pro	Val	Phe	Leu	Val	Lys	Val	Val	Tyr	245	250	255	

Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
260 265 270

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
275 280 285

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
305 310 315 320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
325 330 335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
340 345

<210> 23
<211> 1049
<212> DNA
<213> Arabidopsis thaliana

<400> 23
accaaagcat taatttttat ttttttgttt cagtaaaaga aatgtcatcg tcaaattgga 60
tcgacgacgc ttttacagag gaagagcttc tcgctatcga cgccatcgaa gcttcctaca 120
atttctcccg ttcttcttct tcttcttctt ctgctgctcc gaccgtacaa gctacaacct 180
ccgtccatgg ccacgaggag gatccaaatc aaatcccaa taatatccgt cgccaattgc 240
ctcgttccat cacttcttct acatcttata aacgatttcc tctctcccgt tgccgagcta 300
ggaattttcc agcaatgagg tttggtggta ggattttgta tagcaagact gctactgagg 360
ttgataagcg agcaatgcag cttattaaag ttcttgatac caagagagat gaatctggaa 420
tagcattttgt tggcttggat attgagtggg gaccaagttt tagaaaagggt gttctcccgg 480
ggaaggttgc gactgtccag atatgtgtag atagtaatta ttgtgatgtt atgcatattt 540
ttcattctgg tatccctcaa agtctccaac atcttattga agattcaaca cttgtaaagg 600
taggtattgg aattgatggg gactctgtga agcttttcca tgactatgga gttagtatca 660
aagatgttga ggatctttca gatttagcca accaaaaaat tgggtggagat aaaaaatggg 720
gccttgccct actaactgag acacttgttt gcaaagagct cctgaagcca aacagaatca 780
ggcttgggaa ctgggagttt tctctctgtt caaagcagca gttacaatac gcagcaacgg 840
atgcttatgc ttcatggcat ctttacaagg ttcttaagga ccttctctgat gctgtcagtg 900
gctcataacg tgaaggagga agcttaaagg ttagcctata accccaagag ttagcatcaa 960
atgatatgat acacctaate tagtcaagta gatgcaattc ttgtgaatat tgtatctagt 1020
tctggtccct ttaaccgtcc agaaactag 1049

<210> 24
<211> 288
<212> PRT
<213> Arabidopsis thaliana

<400> 24
Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
1 5 10 15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
20 25 30

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
 35 40 45
 His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
 50 55 60
 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
 65 70 75 80
 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
 85 90 95
 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
 100 105 110
 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
 115 120 125
 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
 130 135 140
 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
 145 150 155 160
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
 165 170 175
 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
 180 185 190
 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
 195 200 205
 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
 210 215 220
 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
 225 230 235 240
 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
 245 250 255
 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
 260 265 270
 His Leu Tyr Lys Val Leu Lys Asp Leu Pro Asp Ala Val Ser Gly Ser
 275 280 285

<210> 25

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> (1)..(22)

<223> Primer

<400> 25

ttcggaaacca ccatcaaaca gg

22

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<221> Misc_feature

<222> (1)..(22)

<223> Primer

<400> 26

ttgctgcaac tctctcaggg cc

22

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Misc_feature

<222> (1)..(21)

<223> Primer

<400> 27

tcagctgttg cccgtctcac t

21

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<221> Misc_feature

<222> (1)..(16)

<223> n=a, c, g, or t

<400> 28

wgtgnagwan canaga

16

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<221> Misc_feature

<222> (1)..(27)

<223> Primer

<400> 29 gctccgcca cataattcaa acaacac	27
<210> 30 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <221> Misc_feature <222> (1)..(22) <223> Primer	
<400> 30 ttcgaaaaca ttacctccga tc	22
<210> 31 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <221> Misc_feature <222> (1)..(25) <223> Primer	
<400> 31 ggcttttgca tttggtatct actag	25
<210> 32 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <221> Misc_feature <222> (1)..(25) <223> Primer	
<400> 32 atgtcatcgt caaattggat cgacg	25
<210> 33 <211> 27 <212> DNA <213> Artificial Sequence	
<220> <221> Misc_feature <222> (1)..(27) <223> Primer	
<400> 33 cgcttatcaa cctcagtagc agtcttg	27

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(24)
<223> Primer

<400> 34
ttatgagcca ctgacagcat cagg

24